Amendment to Specification:

Page 13, line 34 through page 13, line 25

"Percent (%) amino acid sequence identity" is defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the sequence with which it is being compared, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identify, and not considering any conservative substitution as part of the sequence identity. The % identity values used herein are generated by WU-BLAST-2 which was obtained from Altschul et al. (1996), http.//blast.wustl/edu.blast/README.html. WU-BLAST-2 uses several search parameters, most of which are set to the default values. The adjustable parameters are set with the following values: overlap span =1, overlap fraction = 0.125, word threshold (T) = 11. The HSPS and HSPS2 parameters are dynamic values and are established by the program itself depending upon the composition of the particular sequence and composition of the particular database against which the sequence of interest is being searched; however, the values may be adjusted to increase sensitivity. A % amino acid sequence identity value is determined by the number of matching identical residues divided by te total number of residues of the "longer" sequence in the aligned region, multiplied by 100. The 'longer" sequence is the one having the most actual residues in the aligned region (gaps introduced by WU-BLAST-2 to maximize the alignment score are ignored).